

Sequence alignment A
SEQ ID NO: 8

RESULT 29

US-08-883-086-3

; Sequence 3, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
US-08-883-086-3

Query Match 28.7%; Score 210; DB 2; Length 147;
Best Local Similarity 37.1%; Pred. No. 9e-19;
Matches 46; Conservative 27; Mismatches 41; Indels 10; Gaps 3;

QY	21	TFVPWLLSFKRGSAL E E K E N K I L V K E T G Y F F I Y G Q V L Y T D K T Y A M G H L I Q R K K V H V F G D E	80
		: : } : : : : : : : : : : : : :	
Db	31	TEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSRE-----GQ	84
QY	81	LSLVTLFRCIQNMPETLPN---NSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFG	137
		: : : : : : : :	
Db	85	GRQETLFR CIR SMP-SHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA K L N L S P H G T F L G	143
QY	138	ALKL	141
		:	
Db	144	FVKL	147

10/611,399
Sequence search
SEQ ID NO: 8

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	730	99.9	285	2	AAW62460	Aaw62460 Human T c
2	724	99.0	153	3	AAAY97036	Aay97036 Soluble h
3	724	99.0	285	3	AAAY97037	Aay97037 Membrane
4	722	98.8	152	8	ADW80400	Adw80400 Human B l
5	721	98.6	152	8	ADW80398	Adw80398 Human B l
6	715.5	97.9	232	4	AAAY71916	Aay71916 Fusion po
7	711	97.3	285	7	ADK70723	Adk70723 Human B l
8	711	97.3	299	7	ADM77959	Adm77959 Plasmid v
9	709	97.0	152	8	ADK13666	Adk13666 hTNFSF13b
10	708	96.9	152	8	ADK13667	Adk13667 hTNFSF13b
11	689	94.3	152	8	ADK13668	Adk13668 hTNFSF13b
12	684	93.6	152	8	ADK13669	Adk13669 hTNFSF13b
13	684	93.6	152	8	ADK13665	Adk13665 hTNFSF13b
14	676.5	92.5	284	8	ADO05611	Ado05611 Human EXM
15	657	89.9	144	3	AAAY97038	Aay97038 Soluble m
16	657	89.9	147	3	AAB08271	Aab08271 Amino aci
17	657	89.9	183	6	ABP96297	Abp96297 Mouse TNF
18	657	89.9	183	8	ADK13670	Adk13670 Mouse TNF
19	657	89.9	184	5	AAU79151	Aau79151 Rat Neutr
20	657	89.9	184	5	ABG96473	Abg96473 Rat Neutr
21	657	89.9	184	6	AAE37312	Aae37312 Rat neutr
22	657	89.9	184	7	ADJ92651	Adj92651 Rat neutr
23	657	89.9	239	5	ABJ00719	Abj00719 Rat B lym
24	657	89.9	239	5	ABP47221	Abp47221 Human BLy
25	657	89.9	239	5	ABG33580	Abg33580 Rat B Lym

RESULT 16

AAB08271

ID AAB08271 standard; protein; 147 AA.

XX

AC AAB08271;

XX

DT 04-DEC-2000 (first entry)

XX

DE Amino acid sequence of a mouse TNF ligand AGP-3.

XX

KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;

KW type II transmembrane protein; B cell stimulatory factor;

KW inflammatory disorder; immune disorder; rheumatoid arthritis;

KW lupus and graft versus host disease.

XX

OS Mus sp.

XX

PN WO200047740-A2.

XX

PD 17-AUG-2000.

XX

PF 11-FEB-2000; 2000WO-US003653.

XX

PR 12-FEB-1999; 99US-0119906P.

PR 18-NOV-1999; 99US-0166271P.

XX

PA (AMGE-) AMGEN INC.

XX

PI Boyle WJ, Hsu H;

XX

DR WPI; 2000-558217/51.

XX

PT Novel polypeptides comprising tumor necrosis factor ligand family

PT proteins, useful for treating inflammatory and immune disorders, e.g.

PT rheumatoid arthritis.

XX
PS Claim 14; Fig 9; 7lpp; English.
XX
CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand family
CC member. AGP-3 is a type II transmembrane protein, and is a potent B cell
CC stimulatory factor. Expression of AGP-3 correlates to increases in the
CC number of B cells and immunoglobulins produced. AGP-3 proteins,
CC antibodies, and nucleic acids may be used to treat inflammatory and
CC immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and
CC graft versus host disease. The nucleic acids may be used to regulate the
CC expression of an AGP-3 related protein. The AGP-3 proteins, antibodies
CC and nucleic acids are also useful for the detection of AGP-3 agonists,
CC antagonists and characterizing interactions with AGP-3 related proteins
XX
SQ Sequence 147 AA;

Query Match 89.9%; Score 657; DB 3; Length 147;
Best Local Similarity 87.2%; Pred. No. 1.4e-73;
Matches 123; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QDCLQLIADSETPTTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLYTD 60
| | | | | | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 6 QDCLQLIADSDTPTIRKGTYTTFVPWLLSFKRGNALEEKENKIVVRQTGYFFIYSQVLYTD 65
Qy 61 KTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQLAI 120
: | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | | | : | | | |
Db 66 PIFAMGHVIQRKKVHVFGDELSLVTLFRCIQNMPKTLNNSCYSAGIARLEEGDEIQLAI 125
Qy 121 PRENAQISLDGDVTFFGALKL 141
| | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 126 PRENAQISRNGDDTFFGALKL 146

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	645	88.2	266	2	US-09-589-287B-19	Sequence 19, Appl
2	645	88.2	266	2	US-09-879-919-24	Sequence 24, Appl
3	645	88.2	266	2	US-09-588-947A-19	Sequence 19, Appl
4	645	88.2	266	2	US-09-589-286A-19	Sequence 19, Appl
5	645	88.2	266	2	US-09-255-794A-19	Sequence 19, Appl
6	645	88.2	266	2	US-09-507-968D-19	Sequence 19, Appl
7	645	88.2	266	2	US-09-589-285-19	Sequence 19, Appl
8	574	78.5	155	2	US-09-589-287B-23	Sequence 23, Appl
9	574	78.5	155	2	US-09-588-947A-23	Sequence 23, Appl
10	574	78.5	155	2	US-09-589-286A-23	Sequence 23, Appl
11	574	78.5	155	2	US-09-507-968D-23	Sequence 23, Appl
12	574	78.5	155	2	US-09-589-285-23	Sequence 23, Appl
13	574	78.5	290	2	US-10-214-065-8	Sequence 8, Appli
14	540	73.9	289	2	US-09-589-287B-38	Sequence 38, Appl
15	540	73.9	289	2	US-09-588-947A-38	Sequence 38, Appl
16	540	73.9	289	2	US-09-589-286A-38	Sequence 38, Appl
17	540	73.9	289	2	US-09-507-968D-38	Sequence 38, Appl
18	515	70.5	218	2	US-09-911-777-1	Sequence 1, Appli
19	483	66.1	102	2	US-09-911-777-3	Sequence 3, Appli
20	457	62.5	232	2	US-09-911-777-2	Sequence 2, Appli
21	222	30.4	149	2	US-09-854-864-19	Sequence 19, Appl
22	222	30.4	240	2	US-09-854-864-4	Sequence 4, Appli
23	210	28.7	136	2	US-09-589-287B-20	Sequence 20, Appl
24	210	28.7	136	2	US-09-588-947A-20	Sequence 20, Appl
25	210	28.7	136	2	US-09-589-286A-20	Sequence 20, Appl

RESULT 8

US-09-589-287B-23

; Sequence 23, Application US/09589287B
 ; Patent No. 6403770
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu et al.
 ; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
 ; FILE REFERENCE: PF343P3C1
 ; CURRENT APPLICATION NUMBER: US/09/589,287B
 ; CURRENT FILING DATE: 2000-06-08
 ; Prior application data removed - check PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-589-287B-23

Query Match 78.5%; Score 574; DB 2; Length 155;
 Best Local Similarity 81.2%; Pred. No. 1.5e-65;
 Matches 108; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 9 DSETPTIQKGSYTFVPWLLSFKRGSAALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHL 68
 | :: :|||||:|||||:|:||||| ||||| :|||:
 Db 22 DDNGMNLNRNRTYTFVPWLLSFKRGNAALEEKENKIVVRQTGYFFIYSQVLYTDPFAMGHV 81
 Qy 69 IQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQIS 128
 |||||:|||||:|||||:|||||:|||||:|||||
 Db 82 IQRKKVHVFGDELSLVTLFRCIQNMPKTLNNSCYSAGIARLEEGDEIQLAIPRENAQIS 141
 Qy 129 LDGDVTFFGALKL 141
 :|| |||||
 Db 142 RNGDDTFFGALKL 154

RESULT 14

US-09-589-287B-38

; Sequence 38, Application US/09589287B
 ; Patent No. 6403770
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu et al.
 ; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
 ; FILE REFERENCE: PF343P3C1
 ; CURRENT APPLICATION NUMBER: US/09/589,287B
 ; CURRENT FILING DATE: 2000-06-08
 ; Prior application data removed - check PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 38
 ; LENGTH: 289
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-589-287B-38

Query Match 73.9%; Score 540; DB 2; Length 289;
 Best Local Similarity 75.2%; Pred. No. 8.9e-61;
 Matches 106; Conservative 10; Mismatches 5; Indels 20; Gaps 1;

Qy 1 QDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAALEEKENKILVKETGYFFIYGQVLYTD 60
 |||||:| |||||:|:||||| |||||
 Db 168 QDCLQLIADSDTP-----ALEEKENKIVVRQTGYFFIYSQVLYTD 207
 Qy 61 KTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQLAI 120
 :|||:|||||:|||||:|||||:|||||:|||||
 Db 208 PIFAMGHVIQRKKVHVFGDELSLVTLFRCIQNMPKTLNNSCYSAGIARLEEGDEIQLAI 267

Qy 121 PRENAQISLDGDVTFFGALKL 141
 ||||| :|| |||||
 Db 268 PRENAQISRNGDDTFFGALKL 288

RESULT 29

US-08-883-086-3

; Sequence 3, Application US/08883086
 ; Patent No. 6171787
 ; GENERAL INFORMATION:
 ; APPLICANT: WILEY, STEVEN
 ; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
 ; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/883,086
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Porembski, Priscilla E.
 ; REGISTRATION NUMBER: 33,207
 ; REFERENCE/DOCKET NUMBER: 6134.US.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 847-937-0378
 ; TELEFAX: 847-938-2623
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 147 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6171787e
 US-08-883-086-3

Query Match 28.7%; Score 210; DB 2; Length 147;
 Best Local Similarity 37.1%; Pred. No. 9e-19;
 Matches 46; Conservative 27; Mismatches 41; Indels 10; Gaps 3;

Qy 21 TFVPWLLSFKRGSAALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDE 80
 | | | : : | | : : : : | : : | | | : | | : | : : | :
 Db 31 TEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSRE-----GQ 84
 Qy 81 LSLVTLFRCIQNMPETLPN---NSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFG 137
 ||||| : : | : | : ||||| : | : | | : || | : : : | | |
 Db 85 GRQETLFRCI RSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KLNLSPHGTFLG 143
 Qy 138 ALKL 141
 : | |
 Db 144 FVKL 147

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	715.5	97.9	232	3	US-09-302-863-5	Sequence 5, Appli
2	715.5	97.9	232	3	US-09-855-564-5	Sequence 5, Appli
3	657	89.9	147	3	US-09-779-050A-13	Sequence 13, Appl
4	657	89.9	184	3	US-09-929-493-43	Sequence 43, Appl
5	657	89.9	184	4	US-10-270-487-43	Sequence 43, Appl
6	657	89.9	184	6	US-11-054-539-43	Sequence 43, Appl
7	657	89.9	239	3	US-09-880-748-3232	Sequence 3232, Ap
8	657	89.9	239	3	US-09-932-613-177	Sequence 177, App
9	657	89.9	239	3	US-09-932-322-177	Sequence 177, App
10	657	89.9	239	4	US-10-293-418-3232	Sequence 3232, Ap
11	657	89.9	309	3	US-09-929-493-39	Sequence 39, Appl
12	657	89.9	309	3	US-09-880-748-3230	Sequence 3230, Ap
13	657	89.9	309	3	US-09-932-613-175	Sequence 175, App
14	657	89.9	309	3	US-09-932-322-175	Sequence 175, App
15	657	89.9	309	4	US-10-270-487-39	Sequence 39, Appl
16	657	89.9	309	4	US-10-293-418-3230	Sequence 3230, Ap
17	657	89.9	309	5	US-10-861-049-47	Sequence 47, Appl
18	657	89.9	309	6	US-11-016-922-2	Sequence 2, Appli
19	657	89.9	309	6	US-11-021-874-47	Sequence 47, Appl
20	657	89.9	309	6	US-11-080-973-2	Sequence 2, Appli
21	657	89.9	309	6	US-11-054-539-39	Sequence 39, Appl
22	656	89.7	152	3	US-09-929-493-41	Sequence 41, Appl
23	656	89.7	152	4	US-10-270-487-41	Sequence 41, Appl
24	656	89.7	152	6	US-11-054-539-41	Sequence 41, Appl
25	656	89.7	207	3	US-09-880-748-3234	Sequence 3234, Ap

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	657	89.9	239	7	US-11-054-515-3232	Sequence 3232, Ap
2	657	89.9	309	7	US-11-065-669-2	Sequence 2, Appli
3	657	89.9	309	7	US-11-054-515-3230	Sequence 3230, Ap
4	656	89.7	207	7	US-11-054-515-3234	Sequence 3234, Ap
5	645	88.2	266	7	US-11-054-515-3229	Sequence 3229, Ap
6	580	79.3	188	7	US-11-054-515-3235	Sequence 3235, Ap
7	574	78.5	220	7	US-11-054-515-3233	Sequence 3233, Ap
8	574	78.5	290	7	US-11-054-515-3231	Sequence 3231, Ap
9	483	66.1	102	7	US-11-065-669-3	Sequence 3, Appli
10	224	30.6	135	7	US-11-084-647-4	Sequence 4, Appli
11	222	30.4	241	7	US-11-084-647-5	Sequence 5, Appli
12	210	28.7	136	7	US-11-084-647-11	Sequence 11, Appl
13	210	28.7	250	6	US-10-742-634-11	Sequence 11, Appl
14	210	28.7	250	7	US-11-054-515-3239	Sequence 3239, Ap
15	210	28.7	250	7	US-11-084-647-6	Sequence 6, Appli
16	210	28.7	250	7	US-11-136-079-3	Sequence 3, Appli
17	210	28.7	250	7	US-11-242-294-4	Sequence 4, Appli
18	125.5	17.2	96	7	US-11-065-669-4	Sequence 4, Appli
19	100.5	13.7	157	6	US-10-504-389A-55	Sequence 55, Appl
20	95.5	13.1	157	7	US-11-010-954-1	Sequence 1, Appli
21	95.5	13.1	157	7	US-11-053-750-1	Sequence 1, Appli
22	95.5	13.1	157	7	US-11-053-749-1	Sequence 1, Appli
23	95.5	13.1	157	7	US-11-108-001-12	Sequence 12, Appl
24	95.5	13.1	157	7	US-11-170-753-1	Sequence 1, Appli
25	95.5	13.1	157	7	US-11-179-359-1	Sequence 1, Appli

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	96	13.1	235	2	I54490	tumor necrosis fac
2	95.5	13.1	233	1	QWHUN	tumor necrosis fac

3	91.5	12.5	193	2	S06192	tumor necrosis fac
4	91	12.4	234	1	A25451	tumor necrosis fac
5	91	12.4	235	1	QWMSN	tumor necrosis fac
6	91	12.4	235	2	JU0029	tumor necrosis fac
7	90.5	12.4	233	2	S11688	tumor necrosis fac
8	89.5	12.2	233	1	S22052	tumor necrosis fac
9	89.5	12.2	234	1	JQ1344	tumor necrosis fac
10	86.5	11.8	205	1	QWHUX	lymphotoxin alpha
11	81	11.1	185	2	S52715	tumor necrosis fac
12	81	11.1	233	1	S24642	tumor necrosis fac
13	81	11.1	234	1	JH0529	tumor necrosis fac
14	79.5	10.9	889	2	B55123	coatomer complex b
15	78.5	10.7	263	1	H64069	beta-lactamase reg
16	78.5	10.7	281	2	I38707	Fas ligand - human
17	78.5	10.7	942	2	C96574	hypothetical prote
18	78.5	10.7	979	2	D96574	hypothetical prote
19	78	10.7	232	1	S12606	tumor necrosis fac
20	78	10.7	261	2	S53090	CD40 ligand - bovi
21	78	10.7	358	1	W2WL51	E2 protein - human
22	77.5	10.6	279	2	A53062	Fas ligand - mouse
23	77	10.5	261	2	I53476	CD40 ligand - huma
24	76.5	10.5	197	1	JH0309	tumor necrosis fac
25	76	10.4	900	2	T41607	probable vacuolar

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID		Description

1	727	99.5	158	2	Q8IZI4_HUMAN		Q8izi4 homo sapien
2	727	99.5	174	2	Q8IZI5_HUMAN		Q8izi5 homo sapien
3	727	99.5	208	2	Q8IZI6_HUMAN		Q8izi6 homo sapien
4	657	89.9	258	2	Q8BZM8_MOUSE		Q8bzm8 mus musculu
5	657	89.9	309	1	TN13B_MOUSE		Q9wu72 m tumor nec
6	645	88.2	266	2	Q7Z5J2_HUMAN		Q7z5j2 homo sapien
7	582	79.6	288	2	Q8JHJ4_CHICK		Q8jhh4 gallus gall
8	574	78.5	290	2	Q7TQ58_MOUSE		Q7tq58 mus musculu
9	379	51.8	387	2	Q4S0H9_TETNG		Q4s0h9 tetraodon n
10	298.5	40.8	234	2	Q50D53_GASAC		Q50d53 gasterosteu
11	232	31.7	240	2	Q5PQL1_RAT		Q5pql1 rattus norv
12	222	30.4	240	2	Q5F2A4_MOUSE		Q5f2a4 mus musculu
13	222	30.4	241	1	TNF13_MOUSE		Q9d777 mus musculu
14	222	30.4	408	2	Q5F2A1_MOUSE		Q5f2a1 mus musculu
15	222	30.4	410	2	Q8BXS2_MOUSE		Q8bxs2 mus musculu
16	220	30.1	224	2	Q5F2A3_MOUSE		Q5f2a3 mus musculu
17	211	28.9	250	2	Q6FGR7_HUMAN		Q6fgr7 homo sapien
18	210	28.7	146	2	Q6U6I7_HUMAN		Q6u6i7 homo sapien
19	210	28.7	250	1	TNF13_HUMAN		Q75888 homo sapien
20	210	28.7	250	2	Q5U0G8_HUMAN		Q5u0g8 homo sapien
21	210	28.7	250	2	Q6FGN4_HUMAN		Q6fgn4 homo sapien
22	210	28.7	250	2	Q8NFH7_HUMAN		Q8nfh7 homo sapien
23	210	28.7	250	2	Q541E1_HUMAN		Q541e1 homo sapien
24	210	28.7	330	2	Q8IZK7_HUMAN		Q8izk7 homo sapien
25	107	14.6	188	2	Q5BMN0_SALSA		Q5bmno salmo salar